

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: December 2, 2000, 14:54:45 ; Search time 10764.3 Seconds

(without alignments)  
2150.454 Million cell updates/sec

Title: US-09-358-322-1

Sequence: 1 gatcaataataatgaaccca.....taccattactactcagatc 5300

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 1033670 seqs, 2183789903 residues

Total number of hits satisfying chosen parameters: 2067340

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : GenBank:\*

1: gb\_ba1:\*  
2: gb\_ba2:\*  
3: gb\_ba3:\*  
4: gb\_ba4:\*  
5: gb\_ba5:\*  
6: gb\_ba6:\*  
7: gb\_ba7:\*  
8: gb\_ba8:\*  
9: gb\_ba9:\*  
10: gb\_ba10:\*  
11: gb\_ba11:\*  
12: gb\_ba12:\*  
13: gb\_ba13:\*  
14: gb\_ba14:\*  
15: gb\_ba15:\*  
16: gb\_ba16:\*  
17: gb\_ba17:\*  
18: gb\_ba18:\*  
19: gb\_ba19:\*  
20: gb\_ba20:\*  
21: gb\_ba21:\*  
22: gb\_ba22:\*  
23: gb\_ba23:\*  
24: gb\_ba24:\*  
25: gb\_ba25:\*  
26: gb\_ba26:\*  
27: gb\_ba27:\*  
28: gb\_ba28:\*  
29: gb\_ba29:\*  
30: gb\_ba30:\*  
31: gb\_ba31:\*  
32: gb\_ba32:\*  
33: gb\_ba33:\*  
34: gb\_ba34:\*  
35: gb\_ba35:\*  
36: gb\_ba36:\*  
37: gb\_ba37:\*  
38: gb\_ba38:\*  
39: gb\_ba39:\*  
40: gb\_ba40:\*  
41: gb\_ba41:\*  
42: gb\_ba42:\*  
43: gb\_ba43:\*

44: em\_hc97:\*  
45: em\_hc98:\*  
46: em\_hc99:\*  
47: em\_hc100:\*  
48: em\_hc101:\*  
49: em\_hc102:\*  
50: em\_hc103:\*  
51: em\_hc104:\*  
52: em\_hc105:\*  
53: em\_hc106:\*  
54: em\_hc107:\*  
55: em\_hc108:\*  
56: em\_hc109:\*  
57: em\_hc110:\*  
58: em\_hc111:\*  
59: em\_hc112:\*  
60: em\_hc113:\*  
61: em\_hc114:\*  
62: em\_hc115:\*  
63: em\_hc116:\*  
64: em\_hc117:\*  
65: em\_hc118:\*  
66: em\_hc119:\*  
67: em\_hc120:\*  
68: em\_hc121:\*  
69: em\_hc122:\*  
70: em\_hc123:\*  
71: em\_hc124:\*  
72: em\_hc125:\*  
73: em\_hc126:\*  
74: em\_hc127:\*  
75: em\_hc128:\*  
76: em\_hc129:\*  
77: em\_hc130:\*  
78: em\_hc131:\*  
79: em\_hc132:\*  
80: em\_hc133:\*  
81: em\_hc134:\*  
82: em\_hc135:\*  
83: em\_hc136:\*  
84: em\_hc137:\*  
85: em\_hc138:\*  
86: em\_hc139:\*  
87: em\_hc140:\*  
88: em\_hc141:\*  
89: em\_hc142:\*  
90: em\_hc143:\*  
91: em\_hc144:\*  
92: em\_hc145:\*  
93: em\_hc146:\*  
94: em\_hc147:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	314.6	5.9	1306	2	CRPES20	X58342 C.ruminae
2	155.2	2.9	31430	2	RPKX02	AJ235271 Nicketel
3	149.2	2.8	14001	33	PFCOMP1RB	X95276 P.falciparum
4	144.8	2.7	69034	31	AF007261	AF007261 Reclinom
5	140.6	2.7	317511	2	CJ1168X3	AL139076 Campylob
6	138.2	2.6	19517	33	DM037541	U37541 Drosophila
7	137.6	2.6	4601	33	DM011584	U11584 Drosophila
8	136.2	2.6	104992	68	AC005504	AC005504 Plasmodiu
9	136.2	2.6	163226	68	AC004157	AC004157 Plasmodiu
10	133.2	2.5	14867	31	AE001398	AE001398 Plasmodiu
11	128.4	2.4	86827	33	PFMAL3B5	AL034556 Plasmodiu
12	124.2	2.3	86827	33	PFMAL3B5	AL034556 Plasmodiu

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